NOVEL DKR POLYPEPTIDES
Bass, Sullivan, Theill, and Wang
Docket #: A-548A

FIG. 1

1	ATGCAGCGGC	TCGGGGGTAT	TTTGCTGTGT	ACACTGCTGG	CGGCGGCGGT
51	CCCCACTGCT	CCTGCTCCTT	CCCCGACGGT	CACTTGGACT	CCGGCGGAGC
101	CGGGCCCAGC	TCTCAACTAC	CCTCAGGAGG	AAGCTACGCT	CAATGAGATG
151	TTTCGAGAGG	TGGAGGAGCT	GATGGAAGAC	ACTCAGCACA	AACTGCGCAG
201	TGCCGTGGAG	GAGATGGAGG	CGGAAGAAGC	AGCTGCTAAA	ACGTCCTCTG
251	AGGTGAACCT	GGCAAGCTTA	CCTCCCAACT	ATCACAATGA	GACCAGCACG
301	GAGACCAGGG	TGGGAAATAA	CACAGTCCAT	GTGCACCAGG	AAGTTCACAA
351	GATAACCAAC	AACCAGAGTG	GACAGGTGGT	CTTTTCTGAG	ACAGTCATTA
401	CATCTGTAGG	GGATGAAGAA	GGCAAGAGGA	GCCATGAATG	TATCATTGAT
451	GAAGACTGTG	GGCCCACCAG	GTACTGCCAG	TTCTCCAGCT	TCAAGTACAC
501	CTGCCAGCCA	TGCCGGGACC	AGCAGATGCT	ATGCACCCGA	GACAGTGAGT
551	GCTGTGGAGA	CCAGCTGTGT	GCCTGGGGTC	ACTGCACCCA	AAAGGCCACC
601	AAAGGTGGCA	ATGGGACCAT	CTGTGACAAC	CAGAGGGATT	GCCAGCCTGG
651	CCTGTGTTGT	GCCTTCCAAA	GAGGCCTGCT	GTTCCCCGTG	TGCACACCCC
701	TGCCCGTGGA	GGGAGAGCTC	TGCCATGACC	CCACCAGCCA	GCTGCTGGAT
751	CTCATCACCT	GGGAACTGGA	GCCTGAAGGA	GCTTTGGACC	GATGCCCCTG
801	CGCCAGTGGC	CTCCTATGCC	AGCCACACAG	CCACAGTCTG	GTGTACATGT
851	GCAAGCCAGC	CTTCGTGGGC	AGCCATGACC	ACAGTGAGGA	GAGCCAGCTG
901	CCCAGGGAGG	CCCCGGATGA	GTACGAAGAT	GTTGGCTTCA	TAGGGGAAGT
951	GCGCCAGGAG	CTGGAAGACC	TGGAGCGGAG	CCTAGCCCAG	GAGATGGCAT
1001	TTGAGGGGCC	TGCCCCTGTG	GAGTCACTAG	GCGGAGAGGA	GGAGATTTAG

FIG. 2

```
   1  ATGCAGCGGC TTGGGGCCAC CCTGCTGTGC CTGCTGCTGG CGGCGGCGGT
  51  CCCCACGGCC CCCGCGCCCG CTCCGACGGC GACCTCGGCT CCAGTCAAGC
 101  CCGGCCCGGC TCTCAGCTAC CCGCAGGAGG AGGCCACCCT CAATGAGATG
 151  TTCCGCGAGG TTGAGGAACT GATGGAGGAC ACGCAGCACA AATTGCGCAG
 201  CGCGGTGGAA GAGATGGAGG CAGAAGAAGC TGCTGCTAAA GCATCATCAG
 251  AAGTGAACCT GGCAAACTTA CCTCCCAGCT ATCACAATGA GACCAACACA
 301  GACACGAAGG TTGGAAATAA TACCATCCAT GTGCACCGAG AAATTCACAA
 351  GATAACCAAC AACCAGACTG GACAAATGGT CTTTTCAGAG ACAGTTATCA
 401  CATCTGTGGG AGACGAAGAA GGCAGAAGGA GCCACGAGTG CATCATCGAC
 451  GAGGACTGTG GGCCCAGCAT GTACTGCCAG TTTGCCAGCT TCCAGTACAC
 501  CTGCCAGCCA TGCCGGGGCC AGAGGATGCT CTGCACCCGG GACAGTGAGT
 551  GCTGTGGAGA CCAGCTGTGT GTCTGGGGTC ACTGCACCAA AATGGCCACC
 601  AGGGGCAGCA ATGGGACCAT CTGTGACAAC CAGAGGGACT GCCAGCCGGG
 651  GCTGTGCTGT GCCTTCCAGA GAGGCCTGCT GTTCCCTGTG TGCACACCCC
 701  TGCCCGTGGA GGGCGAGCTT TGCCATGACC CCGCCAGCCG GCTTCTGGAC
 751  CTCATCACCT GGGAGCTAGA GCCTGATGGA GCCTTGGACC GATGCCCTTG
 801  TGCCAGTGGC CTCCTCTGCC AGCCCCACAG CCACAGCCTG GTGTATGTGT
 851  GCAAGCCGAC CTTCGTGGGG AGCCGTGACC AAGATGGGGA GATCCTGCTG
 901  CCCAGAGAGG TCCCCGATGA GTATGAAGTT GGCAGCTTCA TGGAGGAGGT
 951  GCGCCAGGAG CTGGAGGACC TGGAGAGGAG CCTGACTGAA GAGATGGCGC
1001  TGGGGGAGCC TGCGGCTGCC GCCGCTGCAC TGCTGGGAGG GGAAGAGATT
1051  TAG
```

FIG. 3

```
  1  ATGATGGCTC TGGGCGCAGC GGGAGCTACC CGGGTCTTTG TCGCGATGGT
 51  AGCGGCGGCT CTCGGCGGCC ACCCTCTGCT GGGAGTGAGC GCCACCTTGA
101  ACTCGGTTCT CAATTCCAAC GCTATCAAGA ACCTGCCCCC ACCGCTGGGC
151  GGCGCTGCGG GGCACCCAGG CTCTGCAGTC AGCGCCGCGC CGGGAATCCT
201  GTACCCGGGC GGGAATAAGT ACCAGACCAT TGACAACTAC CAGCCGTACC
251  CGTGCGCAGA GGACGAGGAG TGCGGCACTG ATGAGTACTG CGCTAGTCCC
301  ACCCGCGGAG GGGACGCGGG CGTGCAAATC TGTCTCGCCT GCAGGAAGCG
351  CCGAAAACGC TGCATGCGTC ACGCTATGTG CTGCCCCGGG AATTACTGCA
401  AAAATGGAAT ATGTGTGTCT TCTGATCAAA ATCATTTCCG AGGAGAAATT
451  GAGGAAACCA TCACTGAAAG CTTTGGTAAT GATCATAGCA CCTTGGATGG
501  GTATTCCAGA AGAACCACCT TGTCTTCAAA AATGTATCAC ACCAAAGGAC
551  AAGAAGGTTC TGTTTGTCTC CGGTCATCAG ACTGTGCCTC AGGATTGTGT
601  TGTGCTAGAC ACTTCTGGTC CAAGATCTGT AAACCTGTCC TGAAAGAAGG
651  TCAAGTGTGT ACCAAGCATA GGAGAAAAGG CTCTCATGGA CTAGAAATAT
701  TCCAGCGTTG TTACTGTGGA GAAGGTCTGT CTTGCCGGAT ACAGAAAGAT
751  CACCATCAAG CCAGTAATTC TTCTAGGCTT CACACTTGTC AGAGACACTA
801  A
```

FIG. 4

1	ATGGCCGCGC	TGATGCGGGT	CAAGGATTCA	TCCCGCTGCC	TTCTCCTACT
51	GGCCGCGGTG	CTGATGGTGG	AGAGCTCACA	GCTAGGCAGC	TCGCGGGCCA
101	AACTCAACTC	CATCAAGTCC	TCTCTAGGAG	GGGAGACTCC	TGCTCAGTCA
151	GCCAACCGAT	CTGCAGGCAT	GAACCAAGGA	CTGGCTTTCG	GCGGCAGTAA
201	GAAGGGCAAA	AGCCTGGGGC	AGGCCTACCC	TTGCAGCAGT	GATAAGGAAT
251	GTGAAGTTGG	AAGATACTGC	CACAGTCCCC	ACCAAGGATC	ATCAGCCTGC
301	ATGCTCTGTA	GGAGGAAAAA	GAAACGATGC	CACAGAGATG	GGATGTGTTG
351	CCCTGGTACC	CGCTGCAATA	ATGGAATCTG	CATCCCAGTC	ACTGAGAGCA
401	TCCTCACCCC	ACATATCCCA	GCTCTGGATG	GCACCCGGCA	TAGAGATCGC
451	AACCATGGTC	ACTATTCCAA	CCATGACCTG	GGATGGCAGA	ATCTAGGAAG
501	GCCACACTCC	AAGATGCCTC	ATATAAAAGG	ACATGAAGGA	GACCCATGCC
551	TACGGTCATC	AGACTGCATT	GATGGGTTTT	GTTGTGCTCG	CCACTTCTGG
601	ACCAAAATCT	GCAAACCAGT	GCTCCATCAG	GGGGAAGTCT	GTACCAAACA
651	ACGCAAGAAG	GGTTCGCACG	GGCTGGAGAT	TTTCCAGAGG	TGTGACTGTG
701	CAAAGGGCCT	GTCCTGCAAA	GTGTGGAAAG	ATGCCACCTA	CTCTTCCAAA
751	GCCAGACTCC	ATGTATGCCA	GAAGATCTGA		

FIG. 5

```
  1  ATGGCCGCGT TGATGCGGAG CAAGGATTCG TCCTGCTGCC TGCTCCTACT
 51  GGCCGCGGTG CTGATGGTGG AGAGCTCACA GATCGGCAGT TCGCGGGCCA
101  AACTCAACTC CATCAAGTCC TCTCTGGGCG GGGAGACGCC TGGTCAGGCC
151  GCCAATCGAT CTGCGGGCAT GTACCAAGGA CTGGCATTCG GCGGCAGTAA
201  GAAGGGCAAA AACCTGGGGC AGGCCTACCC TTGTAGCAGT GATAAGGAGT
251  GTGAAGTTGG GAGGTATTGC CACAGTCCCC ACCAAGGATC ATCGGCCTGC
301  ATGGTGTGTC GGAGAAAAAA GAAGCGCTGC CACCGAGATG GCATGTGCTG
351  CCCCAGTACC CGCTGCAATA ATGGCATCTG TATCCCAGTT ACTGAAAGCA
401  TCTTAACCCC TCACATCCCG GCTCTGGATG GTACTCGGCA CAGAGATCGA
451  AACCACGGTC ATTACTCAAA CCATGACTTG GGATGGCAGA ATCTAGGAAG
501  ACCACACACT AAGATGTCAC ATATAAAAGG GCATGAAGGA GACCCCTGCC
551  TACGATCATC AGACTGCATT GAAGGGTTTT GCTGTGCTCG TCATTTCTGG
601  ACCAAAATCT GCAAACCAGT GCTCCATCAG GGGGAAGTCT GTACCAAACA
651  ACGCAAGAAG GGTTCTCATG GGCTGGAAAT TTTCCAGCGT TGCGACTGTG
701  CGAAGGGCCT GTCTTGCAAA GTATGGAAAG ATGCCACCTA CTCCTCCAAA
751  GCCAGACTCC ATGTGTGTCA GAAAATTTGA
```

FIG. 6

```
  1 ATGGCCGCGT TGATGCGGAG CAAGGATTCG TCCTGCTGCC TGCTCCTACT
 51 GGCCGCGGTG CTGATGGTGG AGAGCTCACA GATCGGCAGT TCGCGGGCCA
101 AACTCAACTC CATCAAGTCC TCTCTGGGCG GGGAGACGCC TGGTCAGGCC
151 GCCAATCGAT CTGCGGGCAT GTACCAAGGA CTGGCATTCG GCGGCAGTAA
201 GAAGGGCAAA AACCTGGGGC AGGCCTACCC TTGTAGCAGT GATAAGGAGT
251 GTGAAGTTGG GAGGTATTGC CACAGTCCCC ACCAAGGATC ATCGGCCTGC
301 ATGGTGTGTC GGAGAAAAAA GAAGCGCTGC CACCGAGATG GCATGTGCTG
351 CCCCAGTACC CGCTGCAATA ATGGGCATGA AGGAGACCCC TGCCTACGAT
401 CATCAGACTG CATTGAAGGG TTTTGCTGTG CTCGTCATTT CTGGACCAAA
451 ATCTGCAAAC CAGTGCTCCA TCAGGGGGAA GTCTGTACCA AACAACGCAA
501 GAAGGGTTCT CATGGGCTGG AAATTTTCCA GCGTTGCGAC TGTGCGAAGG
551 GCCTGTCTTG CAAAGTATGG AAAGATGCCA CCTACTCCTC CAAAGCCAGA
601 CTCCATGTGT GTCAGAAAAT TTGA
```

FIG. 7

```
  1  ATGGTGGCGG CCGTCCTGCT GGGGCTGAGC TGGCTCTGCT CTCCCCTGGG
 51  AGCTCTGGTC CTGGACTTCA ACAACATCAG GAGCTCTGCT GACCTGCATG
101  GGGCCCGGAA GGGCTCACAG TGCCTGTCTG ACACGGACTG CAATACCAGA
151  AAGTTCTGCC TCCAGCCCCG CGATGAGAAG CCGTTCTGTG CTACATGTCG
201  TGGGTTGCGG AGGAGGTGCC AGCGAGATGC CATGTGCTGC CCTGGGACAC
251  TCTGTGTGAA CGATGTTTGT ACTACGATGG AAGATGCAAC CCCAATATTA
301  GAAAGGCAGC TTGATGAGCA AGATGGCACA CATGCAGAAG GAACAACTGG
351  GCACCCAGTC CAGGAAAACC AACCCAAAAG GAAGCCAAGT ATTAAGAAAT
401  CACAAGGCAG GAAGGGACAA GAGGGAGAAA GTTGTCTGAG AACTTTTGAC
451  TGTGGCCCTG GACTTTGCTG TGCTCGTCAT TTTTGGACGA AAATTTGTAA
501  GCCAGTCCTT TTGGAGGGAC AGGTCTGCTC CAGAAGAGGG CATAAAGACA
551  CTGCTCAAGC TCCAGAAATC TTCCAGCGTT GCGACTGTGG CCCTGGACTA
601  CTGTGTCGAA GCCAATTGAC CAGCAATCGG CAGCATGCTC GATTAAGAGT
651  ATGCCAAAAA ATAGAAAAGC TATAA
```

FIG. 8

```
1    MQRLGGILLC TLLAAAVPTA PAPSPTVTWT PAEPGPALNY PQEEATLNEM
51   FREVEELMED TQHKLRSAVE EMEAEEAAAK TSSEVNLASL PPNYHNETST
101  ETRVGNNTVH VHQEVHKITN NQSGQVVFSE TVITSVGDEE GKRSHECIID
151  EDCGPTRYCQ FSSFKYTCQP CRDQQMLCTR DSECCGDQLC AWGHCTQKAT
201  KGGNGTICDN QRDCQPGLCC AFQRGLLFPV CTPLPVEGEL CHDPTSQLLD
251  LITWELEPEG ALDRCPCASG LLCQPHSHSL VYMCKPAFVG SHDHSEESQL
301  PREAPDEYED VGFIGEVRQE LEDLERSLAQ EMAFEGPAPV ESLGGEEEI*
```

FIG. 9

```
1     MQRLGATLLC LLLAAAVPTA PAPAPTATSA PVKPGPALSY PQEEATLNEM
51    FREVEELMED TQHKLRSAVE EMEAEEAAAK ASSEVNLANL PPSYHNETNT
101   DTKVGNNTIH VHREIHKITN NQTGQMVFSE TVITSVGDEE GRRSHECIID
151   EDCGPSMYCQ FASFQYTCQP CRGQRMLCTR DSECCGDQLC VWGHCTKMAT
201   RGSNGTICDN QRDCQPGLCC AFQRGLLFPV CTPLPVEGEL CHDPASRLLD
251   LITWELEPDG ALDRCPCASG LLCQPHSHSL VYVCKPTFVG SRDQDGEILL
301   PREVPDEYEV GSFMEEVRQE LEDLERSLTE EMALGEPAAA AAALLGGEEI
351   *
```

FIG. 10

```
1    MMALGAAGAT RVFVAMVAAA LGGHPLLGVS ATLNSVLNSN AIKNLPPPLG
51   GAAGHPGSAV SAAPGILYPG GNKYQTIDNY QPYPCAEDEE CGTDEYCASP
101  TRGGDAGVQI CLACRKRRKR CMRHAMCCPG NYCKNGICVS SDQNHFRGEI
151  EETITESFGN DHSTLDGYSR RTTLSSKMYH TKGQEGSVCL RSSDCASGLC
201  CARHFWSKIC KPVLKEGQVC TKHRRKGSHG LEIFQRCYCG EGLSCRIQKD
251  HHQASNSSRL HTCQRH*
```

FIG. 11

```
1    MAALMRVKDS SRCLLLLAAV LMVESSQLGS SRAKLNSIKS SLGGETPAQS
51   ANRSAGMNQG LAFGGSKKGK SLGQAYPCSS DKECEVGRYC HSPHQGSSAC
101  MLCRRKKKRC HRDGMCCPGT RCNNGICIPV TESILTPHIP ALDGTRHRDR
151  NHGHYSNHDL GWQNLGRPHS KMPHIKGHEG DPCLRSSDCI DGFCCARHFW
201  TKICKPVLHQ GEVCTKQRKK GSHGLEIFQR CDCAKGLSCK VWKDATYSSK
251  ARLHVCQKI*
```

FIG. 12

```
1    MAALMRSKDS SCCLLLLAAV LMVESSQIGS SRAKLNSIKS SLGGETPGQA
51   ANRSAGMYQG LAFGGSKKGK NLGQAYPCSS DKECEVGRYC HSPHQGSSAC
101  MVCRRKKKRC HRDGMCCPST RCNNGICIPV TESILTPHIP ALDGTRHRDR
151  NHGHYSNHDL GWQNLGRPHT KMSHIKGHEG DPCLRSSDCI EGFCCARHFW
201  TKICKPVLHQ GEVCTKQRKK GSHGLEIFQR CDCAKGLSCK VWKDATYSSK
251  ARLHVCQKI*
```

FIG. 13

```
1    MAALMRSKDS SCCLLLLAAV LMVESSQIGS SRAKLNSIKS SLGGETPGQA
51   ANRSAGMYQG LAFGGSKKGK NLGQAYPCSS DKECEVGRYC HSPHQGSSAC
101  MVCRRKKKRC HRDGMCCPST RCNNGHEGDP CLRSSDCIEG FCCARHFWTK
151  ICKPVLHQGE VCTKQRKKGS HGLEIFQRCD CAKGLSCKVW KDATYSSKAR
201  LHVCQKI*
```

FIG. 14

```
1    MVAAVLLGLS WLCSPLGALV LDFNNIRSSA DLHGARKGSQ CLSDTDCNTR
51   KFCLQPRDEK PFCATCRGLR RRCQRDAMCC PGTLCVNDVC TTMEDATPIL
101  ERQLDEQDGT HAEGTTGHPV QENQPKRKPS IKKSQGRKGQ EGESCLRTFD
151  CGPGLCCARH FWTKICKPVL LEGQVCSRRG HKDTAQAPEI FQRCDCGPGL
201  LCRSQLTSNR QHARLRVCQK IEKL*
```

FIG. 15A

FIG. 15B

FIG. 15C

FIG. 15D

FIG. 16

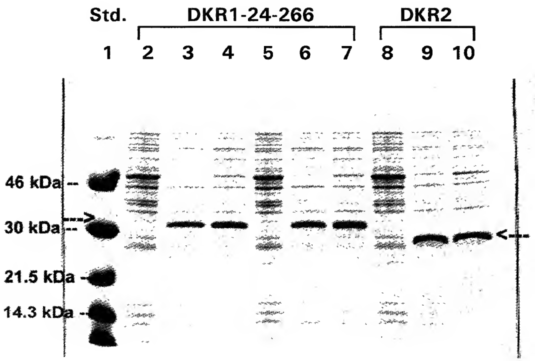

FIG. 17

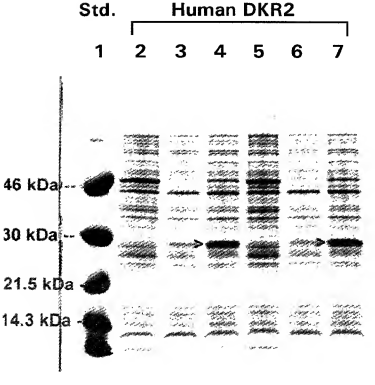

FIG. 18

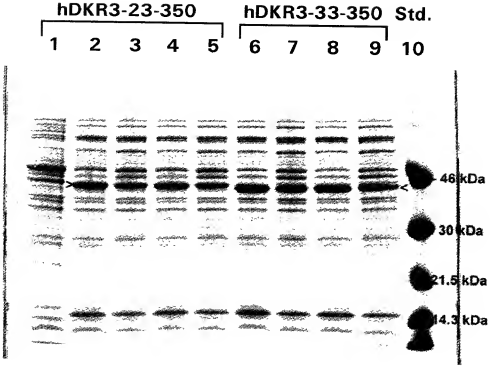
hDKR3-23-350
hDKR3-33-350
Std.
1 2 3 4 5 6 7 8 9 10
46 kDa
30 kDa
21.5 kDa
14.3 kDa

FIG. 19

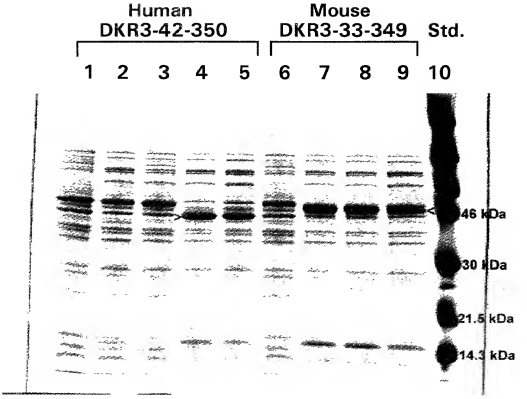
Human
DKR3-42-350
Mouse
DKR3-33-349
Std.
1 2 3 4 5 6 7 8 9 10
46 kDa
30 kDa
21.5 kDa
14.3 kDa

FIG. 20

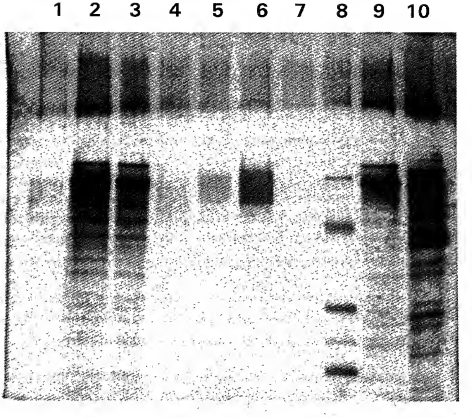

FIG. 21

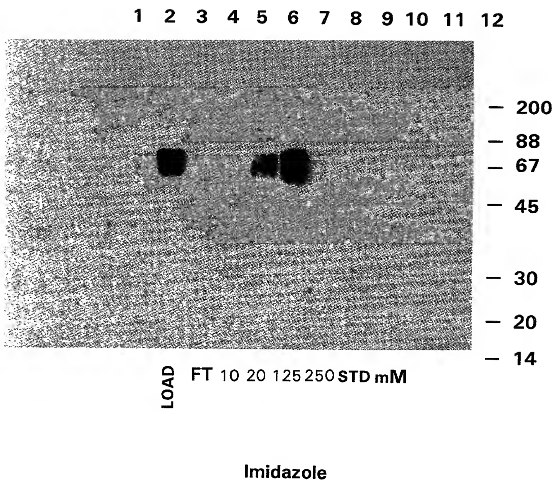
1 2 3 4 5 6 7 8 9 10 11 12
200
88
67
45
30
20
14
LOAD
FT 10 20 125 250 STD mM
Imidazole

FIG. 22

```
1    ATGATGGCTC TGGGTGCTGC TGGTGCTACC CGTGTTTTCG TTGCTATGGT
51   TGCTGCTGCT CTGGGTGGTC ACCCGCTGCT GGGTGTTTCC GCTACCCTGA
101  ACTCCGTTCT GAACTCCAAC GCTATCAAAA ACCTGCCGCC GCCGCTGGGT
151  GGTGCTGCTG GTCACCCGGG TTCCGCTGTT TCCGCTGCTC CGGGTATCCT
201  GTACCCGGGT GGTAACAAAT ACCAGACCAT CGACAACTAC CAGCCGTACC
251  CGTGCGCTGA AGACGAAGAA TGCGGTACCG ACGAATACTG CGCTTCCCCG
301  ACCCGTGGTG GTGACGCTGG TGTTCAGATC TGCCTGGCTT GCCGTAAACG
351  TCGTAAACGT TGCATGCGTC ACGCTATGTG CTGCCCGGGT AACTACTGCA
401  AAAACGGTAT CTGCGTTTCC TCCGACCAGA ACCACTTCCG TGGTGAAATC
451  GAAGAAACCA TCACCGAATC CTTCGGTAAC GACCACTCCA CCCTGGACGG
501  TTACTCCCGT CGTACCACCC TGTCCTCCAA AATGTACCAC ACCAAAGGTC
551  AGGAAGGTTC CGTTTGCCTG CGTTCCTCCG ACTGCGCTTC CGGTCTGTGC
601  TGCGCTCGTC ACTTCTGGTC CAAAATCTGC AAACCGGTTC TGAAAGAAGG
651  TCAGGTTTGC ACCAAACACC GTCGTAAAGG TTCCCACGGT CTGGAAATCT
701  TCCAGCGTTG CTACTGCGGT GAAGGTCTGT CCTGCCGTAT CCAGAAAGAC
751  CACCACCAGG CTTCCAACTC CTCCCGTCTG CACACCTGCC AGCGTCAC
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FIG. 23

```
1    ATGGCTGCTC TGATGCGTTC CAAAGACTCC TCCTGCTGCC TGCTGCTGCT
51   GGCTGCTGTT CTGATGGTTG AATCCTCCCA GATCGGTTCC TCCCGTGCTA
101  AACTGAACTC CATCAAATCC TCCCTGGGTG GTGAAACCCC GGGTCAGGCT
151  GCTAACCGTT CCGCTGGTAT GTACCAGGGT CTGGCTTTCG GTGGTTCCAA
201  AAAAGGTAAA AACCTGGGTC AGGCTTACCC GTGCTCCTCC GACAAAGAAT
251  GCGAAGTTGG TCGTTACTGC CACTCCCCGC ACCAGGGTTC CTCCGCTTGC
301  ATGGTTTGCC GTCGTAAAAA AAAACGTTGC CACCGTGACG GTATGTGCTG
351  CCCGTCCACC CGTTGCAACA ACGGTATCTG CATCCCGGTT ACCGAATCCA
401  TCCTGACCCC GCACATCCCG GCTCTGGACG GTACCCGTCA CCGTGACCGT
451  AACCACGGTC ACTACTCCAA CCACGACCTG GGTTGGCAGA ACCTGGGTCG
501  TCCGCACACC AAAATGTCCC ACATCAAAGG TCACGAAGGT GACCCGTGCC
551  TGCGTTCCTC CGACTGCATC GAAGGTTTCT GCTGCGCTCG TCACTTCTGG
601  ACCAAAATCT GCAAACCGGT TCTGCACCAG GGTGAAGTTT GCACCAAACA
651  GCGTAAAAAA GGTTCCCACG GTCTGGAAAT CTTCCAGCGT TGCGACTGCG
701  CTAAAGGTCT GTCCTGCAAA GTTTGGAAAG ACGCTACCTA CTCCTCCAAA
751  GCTCGTCTGC ACGTTTGCCA GAAAATC
```

FIG. 24

```
1     ATGCAGCGTC TGGGTGCTAC CCTGCTGTGC CTGCTGCTGG CTGCTGCTGT
51    TCCGACCGCT CCGGCTCCGG CTCCGACCGC TACCTCCGCT CCGGTTAAAC
101   CGGGTCCGGC TCTGTCCTAC CCGCAGGAAG AAGCTACCCT GAACGAAATG
151   TTCCGTGAAG TTGAAGAACT GATGGAAGAC ACCCAGCACA AACTGCGTTC
201   CGCTGTTGAA GAAATGGAAG CTGAAGAAGC TGCTGCTAAA GCTTCCTCCG
251   AAGTTAACCT GGCTAACCTG CCGCCGTCCT ACCACAACGA AACCAACACC
301   GACACCAAAG TTGGTAACAA CACCATCCAC GTTCACCGTG AAATCCACAA
351   AATCACCAAC AACCAGACCG GTCAGATGGT TTTCTCCGAA ACCGTTATCA
401   CCTCCGTTGG TGACGAAGAA GGTCGTCGTT CCCACGAATG CATCATCGAC
451   GAAGACTGCG GTCCGTCCAT GTACTGCCAG TTCGCTTCCT TCCAGTACAC
501   CTGCCAGCCG TGCCGTGGTC AGCGTATGCT GTGCACCCGT GACTCCGAAT
551   GCTGCGGTGA CCAGCTGTGC GTTTGGGGTC ACTGCACCAA AATGGCTACC
601   CGTGGTTCCA ACGGTACCAT CTGCGACAAC CAGCGTGACT GCCAGCCGGG
651   TCTGTGCTGC GCTTTCCAGC GTGGTCTGCT GTTCCCGGTT TGCACCCCGC
701   TGCCGGTTGA AGGTGAACTG TGCCACGACC CGGCTTCCCG TCTGCTGGAC
751   CTGATCACCT GGGAACTGGA ACCGGACGGT GCTCTGGACC GTTGCCCGTG
801   CGCTTCCGGT CTGCTGTGCC AGCCGCACTC CCACTCCCTG GTTTACGTTT
851   GCAAACCGAC CTTCGTTGGT TCCCGTGACC AGGACGGTGA AATCCTGCTG
901   CCGCGTGAAG TTCCGGACGA ATACGAAGTT GGTTCCTTCA TGGAAGAAGT
951   TCGTCAGGAA CTGGAAGACC TGGAACGTTC CCTGACCGAA GAAATGGCTC
1001  TGGGTGAACC GGCTGCTGCT GCTGCTGCTC TGCTGGGTGG TGAAGAAATC
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FIG. 25

```
1    ATGGTTGCTG CTGTTCTGCT GGGTCTGTCC TGGCTGTGCT CCCCGCTGGG
51   TGCTCTGGTT CTGGACTTCA ACAACATCCG TTCCTCCGCT GACCTGCACG
101  GTGCTCGTAA AGGTTCCCAG TGCCTGTCCG ACACCGACTG CAACACCCGT
151  AAATTCTGCC TGCAGCCGCG TGACGAAAAA CCGTTCTGCG CTACCTGCCG
201  TGGTCTGCGT CGTCGTTGCC AGCGTGACGC TATGTGCTGC CCGGGTACCC
251  TGTGCGTTAA CGACGTTTGC ACCACCATGG AAGACGCTAC CCCGATCCTG
301  GAACGTCAGC TGGACGAACA GGACGGTACC CACGCTGAAG GTACCACCGG
351  TCACCCGGTT CAGGAAAACC AGCCGAAACG TAAACCGTCC ATCAAAAAAT
401  CCCAGGGTCG TAAAGGTCAG GAAGGTGAAT CCTGCCTGCG TACCTTCGAC
451  TGCGGTCCGG GTCTGTGCTG CGCTCGTCAC TTCTGGACCA AAATCTGCAA
501  ACCGGTTCTG CTGGAAGGTC AGGTTTGCTC CCGTCGTGGT CACAAAGACA
551  CCGCTCAGGC TCCGGAAATC TTCCAGCGTT GCGACTGCGG TCCGGGTCTG
601  CTGTGCCGTT CCCAGCTGAC CTCCAACCGT CAGCACGCTC GTCTGCGTGT
651  TTGCCAGAAA ATCGAAAAAC TG
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